

SEQUENCE LISTING

<110> Skeiky, Yasir
 Reed, Steven
 Alderson, Mark
 Corixa Corporation

<120> Fusion Proteins of Mycobacterium Tuberculosis

<130> 014058-009050US

<140> US 09/597,796

<141> 2000-06-20

<150> US 09/056,556

<151> 1998-04-07

<150> US 09/223,040

<151> 1998-12-30

<150> WO PCT/US99/07717

<151> 1999-04-07

<150> US 09/287,849

<151> 1999-04-07

<150> US 60/158,338

<151> 1999-10-07

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<170> PatentIn Ver. 2.1

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 35 40 45
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 Met Ser Ser Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly
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 Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val
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 1 5 10 15
 Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly Pro Gly Ser Ala Ser
 20 25 30
 Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val Ala Ser Asp Leu Phe
 35 40 45

Gly	Gly	Gln	Gly	Gly	Thr	Pro	Arg	Ala	Val	Pro	Gly	Arg	Val	Val	Ala
530						535					540				
Leu	Gly	Gln	Thr	Val	Gln	Ala	Ser	Asp	Ser	Leu	Thr	Gly	Ala	Glu	Glu
545					550					555					560
Thr	Leu	Asn	Gly	Leu	Ile	Gln	Phe	Asp	Ala	Ala	Ile	Gln	Pro	Gly	Asp
			565						570					575	
Ser	Gly	Gly	Pro	Val	Val	Asn	Gly	Leu	Gly	Gln	Val	Val	Gly	Met	Asn
			580					585					590		
Thr	Ala	Ala	Ser												
			595												

<210> 11
 <211> 2287
 <212> DNA
 <213> Mycobacterium tuberculosis

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:fusion
 protein Ra12-TbH9-Ra35 (MTB72F)

<220>
 <221> modified_base
 <222> (30)
 <223> n = g, a, c or t

<220>
 <221> modified_base
 <222> (33)
 <223> n = g, a, c or t

<220>
 <221> CDS
 <222> (42)..(2231)
 <223> MTB72F

<220>
 <221> modified_base
 <222> (2270)
 <223> n = g, a, c or t

<400> 11
 tctagaaata attttgttta ctttaagaan ganatataca tatgcatcac catcaccatc 60
 acacggccgc gtccgataac ttccagctgt cccaggggtg gcagggattc gccattccga 120
 tcgggcaggc gatggcgatc gcgggccaga tccgatcggg tgggggggtca cccaccgttc 180
 atatcgggcc taccgccttc ctcggttgg gtgttgcga caacaacggc aacggcgcac 240
 gagtccaacg cgtggtcggg agcgctcgg cggaagtct cggcatctcc accggcgacg 300
 tgatcaccgc ggtcgacggc gtcctgatca actcggccac cgcgatggcg gacgcgtta 360
 acgggcatca tcccggtgac gtcctctcgg tgacctggca aaccaagtcg ggcggcacgc 420
 gtacagggaa cgtgacattg gccgaggac ccccgccga attcatggtg gatttcgggg 480
 cgttaccacc ggagatcaac tccgcgagga tgtacgccgg cccgggttcg gcctcgctgg 540
 tggccgcggc tcagatgtgg gacagcgtgg cgagtgaact gttttcggcc gcgtcggcgt 600
 ttcagtcggt ggtctgggg ctgacggtgg ggtcgtggat aggttcgtcg gcgggtctga 660
 tggtggcggc ggcctcgccg tatgtggcgt ggtgagcgt caccgcgggg caggccgagc 720
 tgaccccgcc ccaggtccgg gttgctgcgg cggcctacga gacggcgtat gggctgacgg 780
 tgcccccgcc ggtgatcgcc gagaaccgtg ctgaactgat gattctgata gcgaccaacc 840
 tcttggggca aaacaccccg gcgatcgcg tcaacgaggc cgaatacggc gagatgtggg 900
 cccaagacgc cgccgcgatg tttggctacg ccgcggcgac ggcgacggcg acggcgacgt 960
 tgctgccgtt cgaggaggcg ccggagatga ccagcgcggg tgggctcctc gagcaggccg 1020

```

ccgcggtcga ggaggcctcc gacaccgccg cggcgaacca gttgatgaac aatgtgcccc 1080
aggcgctgca acagctggcc cagcccacgc agggcaccac gccttcttcc aagctgggtg 1140
gcctgtggaa gacggtctcg ccgcacggtg cggcgatcag caacatggtg tcgatggcca 1200
acaaccacat gtcgatgacc aactcgggtg tgctgatgac caacaccttg agctcgatgt 1260
tgaagggtt tgctccggcg gcggcccgcc aggcggtgca aaccgcggcg caaaacgggg 1320
tccgggcat gagctcgctg ggcagctcgc tgggttcttc gggctcgggc ggtggggtgg 1380
ccgccaactt gggcggggcg gcctcggctg gttcgttctc ggtgccgcag gcctggggcg 1440
cggccaacca ggcagtcacc ccggcggcgc gggcgctgcc gctgaccagc ctgaccagcg 1500
ccgcggaag agggcccggg cagatgctgg gcgggctgcc ggtggggcag atgggcgcca 1560
gggcccgttg tgggctcagt ggtgtgctgc gtgttcggc gcgacctat gtgatgccgc 1620
attctccggc agccggcgat atcgccccgc cggccttgct gcaggaccgg ttcgccgact 1680
tccccgcgt gcccctcgac ccgtccgcga tggctgcccc agtggggcca caggtggtca 1740
acatcaaac caaactgggc tacaacaacg ccgtgggcgc cgggaccggc atcgctcatc 1800
atcccaacg gtctgtgctg accaacaacc acgtgatcgc gggcgccacc gacatcaatg 1860
cgttcagcgt cggctccggc caaacctacg gcgtcgatgt ggtcgggtat gaccgcaccc 1920
aggatgtcgc ggtgctgcag ctgcgcgggt cgggtggcct gccgtcggcg gcgatcgggt 1980
gcggcgctgc ggttggtgag cccgtcgtcg cgatgggcaa cagcgggtggg cagggcgga 2040
cgccccgtgc ggtgcctggc aggggtggtc cgctcggcca aaccgtgcag gcgtcggatt 2100
cgctgaccgg tgccgaagag acattgaacg ggttgatcca gttcgatgcc gcgatccagc 2160
ccggtgattc gggcgggccc gtcgtcaacg gcctaggaca ggtggtcgg atgaacacgg 2220
ccgcgtccta ggatatccat cacactggcg gccgtcgcag cagatccggn tgaacaaag 2280
ccccgaaa

```

```

<210> 12
<211> 729
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: fusion
        protein Ral2-TbH9-Ra35 (MTB72F)

```

```

<400> 12
Met His His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
  1          5          10          15
Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
          20          25          30
Ile Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile
          35          40          45
Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn
          50          55          60
Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu
          65          70          75          80
Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile
          85          90          95
Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly
          100          105          110
Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr
          115          120          125
Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Met Val Asp
          130          135          140
Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly
          145          150          155          160
Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val
          165          170          175
Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp
          180          185          190
Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val
          195          200          205
Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln
          210          215          220

```

Ala	Glu	Leu	Thr	Ala	Ala	Gln	Val	Arg	Val	Ala	Ala	Ala	Ala	Tyr	Glu
225					230					235					240
Thr	Ala	Tyr	Gly	Leu	Thr	Val	Pro	Pro	Pro	Val	Ile	Ala	Glu	Asn	Arg
				245						250				255	
Ala	Glu	Leu	Met	Ile	Leu	Ile	Ala	Thr	Asn	Leu	Leu	Gly	Gln	Asn	Thr
			260					265					270		
Pro	Ala	Ile	Ala	Val	Asn	Glu	Ala	Glu	Tyr	Gly	Glu	Met	Trp	Ala	Gln
		275					280					285			
Asp	Ala	Ala	Ala	Met	Phe	Gly	Tyr	Ala	Ala	Ala	Thr	Ala	Thr	Ala	Thr
	290					295					300				
Ala	Thr	Leu	Leu	Pro	Phe	Glu	Glu	Ala	Pro	Glu	Met	Thr	Ser	Ala	Gly
305					310					315					320
Gly	Leu	Leu	Glu	Gln	Ala	Ala	Ala	Val	Glu	Glu	Ala	Ser	Asp	Thr	Ala
				325					330					335	
Ala	Ala	Asn	Gln	Leu	Met	Asn	Asn	Val	Pro	Gln	Ala	Leu	Gln	Gln	Leu
			340					345					350		
Ala	Gln	Pro	Thr	Gln	Gly	Thr	Thr	Pro	Ser	Ser	Lys	Leu	Gly	Gly	Leu
		355					360						365		
Trp	Lys	Thr	Val	Ser	Pro	His	Arg	Ser	Pro	Ile	Ser	Asn	Met	Val	Ser
	370					375						380			
Met	Ala	Asn	Asn	His	Met	Ser	Met	Thr	Asn	Ser	Gly	Val	Ser	Met	Thr
385					390					395					400
Asn	Thr	Leu	Ser	Ser	Met	Leu	Lys	Gly	Phe	Ala	Pro	Ala	Ala	Ala	Arg
				405					410					415	
Gln	Ala	Val	Gln	Thr	Ala	Ala	Gln	Asn	Gly	Val	Arg	Ala	Met	Ser	Ser
			420					425					430		
Leu	Gly	Ser	Ser	Leu	Gly	Ser	Ser	Gly	Leu	Gly	Gly	Gly	Val	Ala	Ala
		435					440					445			
Asn	Leu	Gly	Arg	Ala	Ala	Ser	Val	Gly	Ser	Leu	Ser	Val	Pro	Gln	Ala
	450					455					460				
Trp	Ala	Ala	Ala	Asn	Gln	Ala	Val	Thr	Pro	Ala	Ala	Arg	Ala	Leu	Pro
465					470					475					480
Leu	Thr	Ser	Leu	Thr	Ser	Ala	Ala	Glu	Arg	Gly	Pro	Gly	Gln	Met	Leu
				485				490						495	
Gly	Gly	Leu	Pro	Val	Gly	Gln	Met	Gly	Ala	Arg	Ala	Gly	Gly	Gly	Leu
			500					505					510		
Ser	Gly	Val	Leu	Arg	Val	Pro	Pro	Arg	Pro	Tyr	Val	Met	Pro	His	Ser
		515					520					525			
Pro	Ala	Ala	Gly	Asp	Ile	Ala	Pro	Pro	Ala	Leu	Ser	Gln	Asp	Arg	Phe
	530					535					540				
Ala	Asp	Phe	Pro	Ala	Leu	Pro	Leu	Asp	Pro	Ser	Ala	Met	Val	Ala	Gln
545					550					555					560
Val	Gly	Pro	Gln	Val	Val	Asn	Ile	Asn	Thr	Lys	Leu	Gly	Tyr	Asn	Asn
				565					570					575	
Ala	Val	Gly	Ala	Gly	Thr	Gly	Ile	Val	Ile	Asp	Pro	Asn	Gly	Val	Val
			580				585						590		
Leu	Thr	Asn	Asn	His	Val	Ile	Ala	Gly	Ala	Thr	Asp	Ile	Asn	Ala	Phe
		595					600					605			
Ser	Val	Gly	Ser	Gly	Gln	Thr	Tyr	Gly	Val	Asp	Val	Val	Gly	Tyr	Asp
	610					615					620				
Arg	Thr	Gln	Asp	Val	Ala	Val	Leu	Gln	Leu	Arg	Gly	Ala	Gly	Gly	Leu
625					630					635					640
Pro	Ser	Ala	Ala	Ile	Gly	Gly	Gly	Val	Ala	Val	Gly	Glu	Pro	Val	Val
				645					650					655	
Ala	Met	Gly	Asn	Ser	Gly	Gly	Gln	Gly	Gly	Thr	Pro	Arg	Ala	Val	Pro
			660				665						670		
Gly	Arg	Val	Val	Ala	Leu	Gly	Gln	Thr	Val	Gln	Ala	Ser	Asp	Ser	Leu
		675					680					685			
Thr	Gly	Ala	Glu	Glu	Thr	Leu	Asn	Gly	Leu	Ile	Gln	Phe	Asp	Ala	Ala
	690					695					700				

Ile Gln Pro Gly Asp Ser Gly Gly Pro Val Val Asn Gly Leu Gly Gln
 705 710 715 720
 Val Val Gly Met Asn Thr Ala Ala Ser
 725

<210> 13
 <211> 500
 <212> DNA
 <213> Mycobacterium tuberculosis

<220>
 <223> Mtb8.4 (DPV)

<400> 13
 cgtggcaatg tcgttgaccg tcggggccgg ggtcgctcc gcagatcccg tggacgcggt 60
 cattaacacc acctgcaatt acgggcaggt agtagctgcg ctcaacgcga cggatccggg 120
 ggctgccgca cagttcaacg cctcaccggt ggcgagtc tatttgcgca atttcctcgc 180
 cgcaccgcca cctcagcgcg ctgccatggc cgcgcaattg caagctgtgc cggggggcggc 240
 acagtacatc ggcttgtcg agtcggttgc cggctcctgc aacaactatt aagcccatgc 300
 gggccccatc ccgcgaccgc gcacgcgcgc cgggggtagg ccagattgcc ccgctcctca 360
 acgggcccga tcccgcgacc cggcatcgtc gccggggcta ggccagattg ccccgctcct 420
 caacggggcg catctcgtgc cgaattcctg cagcccgggg gatccactag ttctagagcg 480
 gccgccaccg cgggtggagct 500

<210> 14
 <211> 96
 <212> PRT
 <213> Mycobacterium tuberculosis

<220>
 <223> Mtb8.4 (DPV)

<400> 14
 Val Ala Met Ser Leu Thr Val Gly Ala Gly Val Ala Ser Ala Asp Pro
 1 5 10 15
 Val Asp Ala Val Ile Asn Thr Thr Cys Asn Tyr Gly Gln Val Val Ala
 20 25 30
 Ala Leu Asn Ala Thr Asp Pro Gly Ala Ala Ala Gln Phe Asn Ala Ser
 35 40 45
 Pro Val Ala Gln Ser Tyr Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro
 50 55 60
 Gln Arg Ala Ala Met Ala Ala Gln Leu Gln Ala Val Pro Gly Ala Ala
 65 70 75 80
 Gln Tyr Ile Gly Leu Val Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr
 85 90 95

<210> 15
 <211> 585
 <212> DNA
 <213> Mycobacterium tuberculosis

<220>
 <223> Mtb9.8 (MSL)

<400> 15
 tggattccga tagcgggttc ggcccctcga cgggcgacca cggcgcgag gcctccgaac 60
 gggggggccgg gacgctggga ttccgggga ccgcaaccaa agaacgccgg gtccggggcg 120
 tcgggctgac cgcactggcc ggtgatgagt tcggcaacgg cccccggatg ccgatggtgc 180

```

cggggacctg ggagcagggc agcaacgagc ccgaggcgcc cgacggatcg gggagagggg 240
gaggcgacgg cttaccgcac gacagcaagt aaccgaattc cgaatcacgt ggacccttac 300
gggtcgaaag gagagatgtt atgagccttt tggatgctca tatcccacag ttggtggcct 360
cccagtcggc gtttgccgcc aaggcggggc tgatgcgga cagcatcggt caggccgagc 420
aggcgcgcat gtcggctcag gcgtttcacc agggggagtc gtcggcgcg tttcaggccg 480
cccatgcccc gtttggtggc gcggccgcc aagtcaacac cttgttggt gtcgcgcagg 540
cgaatctggg tgaggccgcc ggtacctatg tggccgccga tgctg 585

```

```

<210> 16
<211> 97
<212> PRT
<213> Mycobacterium tuberculosis

```

```

<220>
<223> Mtb9.8 (MSL)

```

```

<400> 16
Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser
 1          5          10          15
Ala Phe Ala Ala Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala
 20          25          30
Glu Gln Ala Ala Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser
 35          40          45
Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala Ala Ala Ala Lys
 50          55          60
Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala
 65          70          75          80
Gly Thr Tyr Val Ala Ala Asp Ala Ala Ala Ser Thr Tyr Thr Gly
 85          90          95
Phe

```

```

<210> 17
<211> 1742
<212> DNA
<213> Mycobacterium tuberculosis

```

```

<220>
<223> Mtb9.9A (MTI, MTI-A)

```

```

<220>
<221> modified_base
<222> (1)..(1742)
<223> n = g, a, c or t

```

```

<400> 17
ccgtctcttt tcaacgtcat aagttcgggt ggccagtcgg ccgcgcggtc atatggcacc 60
aataacgcgt gtcccatgga taccgggacc gcacgacggt agagcggatc agcgagccg 120
gtgccgaaca ctaccgcgtc cacgtcagc cctgccgctg tgcggaagat cgagcccagg 180
ttctcatggt cgtaacgcc ttccaacact gcgacgggtg gcgccccggc gaccacctga 240
gcaacgctcg gctccggcac ccggcgcgcg gctgccaaac cccacgatt gagatggaag 300
ccgatcaccg gtgccatgac atcagccgac gctcgatagt acggcgcgcc gacaccggcc 360
agatcatcct tgagctcggc cagccggcgg tcggtgccga acagcgccag cggcgtgaac 420
cgtgaggcca gcatgcgctg caccaccagc acacctcgg cgatcaccaa cgccttgccg 480
gtcggcagat cgggacnacn gtcgatgctg ttcagggtcac ggaaatcgtc gagccgtggg 540
tcgtcgggat cgcagacgtc ctgaacatcg aggcgctcgg ggtgctgggc acaacggcct 600
tcggcacagg gctttcgtcg accagagcca gcatcagatc ggcgcgctg cgcaggatgt 660
cacgtcgtcg gcggttcagc gtcgcgagcc gctcagccag ccaactcttg agagagccgt 720
tgctgggatt aattgggaga ggaagacagc atgtcgttcg tgaccacaca gccggaagcc 780
ctggcagctg cggcggcgaa cctacagggt attggcacga caatgaacgc ccagaacgcg 840

```

```

gccgcggctg ctccaaccac cggagtagtg cccgcagccg ccgatgaagt atcagcgctg 900
accgcggctc agtttgctgc gcacgcgcag atgtaccaa cggtcagcgc ccaggccgcg 960
gccattcacg aaatgttcgt gaacacgctg gtggccagtt ctggctcata cgcggccacc 1020
gaggcggcca acgcagccgc tgccggctga acgggctcgc acgaacctgc tgaaggagag 1080
ggggaacatc cggagttctc gggtcagggg ttgcgccagc gccagccga ttcagntatc 1140
ggcgctcata acagcagacg atctaggcat tcagtactaa ggagacaggc aacatggcct 1200
cacgttttat gacggatccg catgcgatgc gggacatggc gggccgtttt gaggtgcacg 1260
cccagacggg ggaggacgag gctcgccgga tgtgggcgtc cgcgcaaaac atttccgggtg 1320
cgggctggag tggcatggcc gaggcgacct cgctagacac catgacctag atgaatcagg 1380
cgtttcgcaa catcgtgaac atgctgcacg ggggtgcgtga cgggctgggt cgcgacgcca 1440
acaantacga acagcaagag caggcctccc agcagatcct gagcagntag cgccgaaagc 1500
cacagctgng tacgntttct cacattagga gaacaccaat atgacgatta attaccagtt 1560
cggggacgtc gacgctcatg gcgcatgat ccgcgctcag gcggcgctcg ttgaggcgga 1620
gcatcaggcc atcgttcgtg atgtgttggc cgcgggtgac ttttggggcg gcgccggttc 1680
gggtggttgc caggagttca ttaccagtt gggccgtaac ttccagggtga tctacgagca 1740
gg

```

<210> 18
 <211> 94
 <212> PRT
 <213> Mycobacterium tuberculosis

<220>
 <223> Mtb9.9A (MTI, MTI-A)

```

<400> 18
Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met
 1           5           10           15
Ile Arg Ala Leu Ala Gly Leu Leu Glu Ala Glu His Gln Ala Ile Ile
      20           25           30
Ser Asp Val Leu Thr Ala Ser Asp Phe Trp Gly Gly Ala Gly Ser Ala
      35           40           45
Ala Cys Gln Gly Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile
      50           55           60
Tyr Glu Gln Ala Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn
      65           70           75           80
Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala
      85           90

```

<210> 19
 <211> 1200
 <212> DNA
 <213> Mycobacterium tuberculosis

<220>
 <223> MTB40 (HTCC#1) cDNA

```

<400> 19
caggcatgag cagagcgttc atcatcgatc caacgatcag tgccattgac ggcttgtacg 60
accttctggg gattggaata cccaaccaag ggggtatcct ttactcctca ctagagtact 120
tcgaaaaagc cctggaggag ctggcagcag cgtttccggg tgatggctgg ttaggttcgg 180
ccgcggacaa atacgccggc aaaaaccgca accacgtgaa ttttttccag gaactggcag 240
acctcgatcg tcagctcatc agcctgatcc acgaccaggc caacgcggtc cagacgacct 300
gagacatcct ggagggcgcc aagaaaggtc tcgagttcgt gcgcccgggt gctgtggacc 360
tgacctacat cccggtcgtc gggcacgccc tategccgcg cttccaggcg ccgttttgcg 420
cgggcgcgat ggccgtagtg ggcggcgcgc ttgcctactt ggctcgtgaaa acgctgatca 480
acgcgactca actcctcaaa ttgcttgcca aattggcgga gttggtcgcg gccgccattg 540
cggacatcat ttcggatgtg gcggacatca tcaagggcac cctcggagaa gtgtgggagt 600
tcatcacaaa cgcgctcaac ggcctgaaag agctttggga caagctcacg ggggtgggtga 660

```

```

ccggactggt ctctcgaggg tggtcgaacc tggagtcctt ctttgcgggc gtccccgggt 720
tgaccggcgc gaccagcggc ttgtcgcaag tgactggctt gttcgggtgcg gccgggtctgt 780
ccgcatcgtc gggcttggt caccgcgata gcctggcgag ctcagccagc ttgcccgccc 840
tggccggcat tgggggcggg tccggttttg ggggcttgcc gagcctgggt caggtccatg 900
ccgcctcaac tcggcaggcg ctacggcccc gagctgatgg cccggtcggc gccgctgccg 960
agcaggtcgg cgggcagtcg cagctggtct ccgcgccaggg ttcccaaggt atgggcggac 1020
ccgtaggcat gggcggcatg caccctctt cgggggcgtc gaaagggacg acgacgaaga 1080
agtactcgga aggcgcggcg gcgggcactg aagacgccga gcgcgcgcca gtcgaagctg 1140
acgcgggcgg tgggcaaaaag gtgctggtac gaaacgtcgt ctaacggcat ggcgagccaa 1200

```

```

<210> 20
<211> 392
<212> PRT
<213> Mycobacterium tuberculosis

```

```

<220>
<223> MTB40 (HTCC#1)

```

```

<400> 20
Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala Ile Asp Gly
1          5          10          15
Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly Gly Ile Leu
20          25          30
Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu Leu Ala Ala
35          40          45
Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala
50          55          60
Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu
65          70          75          80
Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln
85          90          95
Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly Leu Glu Phe Val
100         105         110
Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val Gly His Ala
115         120         125
Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala Met Ala Val
130         135         140
Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu Ile Asn Ala
145         150         155         160
Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala
165         170         175
Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Thr
180         185         190
Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
195         200         205
Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
210         215         220
Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
225         230         235         240
Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala
245         250         255
Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
260         265         270
Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe
275         280         285
Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln
290         295         300
Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln
305         310         315         320

```

Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met
325 330 335
Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser
340 345 350
Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr
355 360 365
Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln
370 375 380
Lys Val Leu Val Arg Asn Val Val
385 390

<210> 21
<211> 1441
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> MTB41 (MTCC#2)

<400> 21
gaggttgctg gcaatggatt tcgggctttt acctcgggaa gtgaattcaa gccgaatgta 60
ttcgggtccg gggccggagt cgatgctagc cgccgcgggc gcctgggacg gtgtggccgc 120
ggagttgact tccgccgcgg tctcgtagtg atcgggtggtg tcgacgctga tcgttgagcc 180
gtggatgggg ccggcgggcg ccgcgatggc ggccgcgcca acgcccgtatg tgggggtggct 240
ggccgccacg gcggcgctgg cgaaggagac ggccacacag gcgagggcag cggcggaagc 300
gtttgggacg gcgttcgcga tgacgggtgc accatccctc gtcgcgcca accgcagccg 360
gttgatgtcg ctggtcgcgg cgaacattct ggggcaaaac agtgcggcga tcgcggtac 420
ccaggccgag tatgccgaaa tgtgggcccc agacgctgcc gtgatgtaca gctatgaggg 480
ggcatctgcg gccgcgtcgg cgttgccgcc gttcactcca cccgtgcaag gcaccggccc 540
ggccggggccc gcggccgcag ccgcggcgac ccaagccgcc ggtgcgggcg ccgttgcgga 600
tgcacaggcg acaactggccc agctgcccc gggtatcctg agcgacattc tgtccgcatt 660
ggccgccaac gctgatccgc tgacatcggg actggtgggg atcgcgctga ccctcaacc 720
gcaagtccga tccgctcagc cgatagtgat cccaccccc ataggggaat tggacgtgat 780
cgcgctctac attgcatcca tcgcgaccgg cagcattgcg ctgcgcatca cgaacacggc 840
cagaccctgg cacatcggcc tatacgggaa cgccggcggg ctgggaccga cgcagggcca 900
tccactgagt tcggcgaccg acgagccgga gccgcaactg ggccccttcg ggggcgcggc 960
gccggtgtcc gcgggcgtcg gccacgcagc attagtcgga gcgttgctcg tgccgcacag 1020
ctggaccacg gccgccccgg agatccagct cgccgttcag gcaacaccca ccttcagctc 1080
cagcgcggcg gccgaccga cgccctaaa cgggatgccg gcaggcctgc tcagcgggat 1140
ggctttggcg agcctggccg cagcggcac gacgggcggt ggcggcaccc gtagcggcac 1200
cagcactgac ggccaagagg acggccgcaa acccccggta gttgtgatta gagagcagcc 1260
gccgcccgga aacccccgc ggtaaaagtc cggcaaccgt tcgtcgccgc gcgaaaatg 1320
cctggtgagc gtggctatcc gacgggccgt tcacaccgct tgtagtagcg tacggctatg 1380
gacgacggtg tctggattct cggcggtat cagagcgatt ttgctcgcaa cctcagcaaa 1440
g 1441

<210> 22
<211> 423
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> MTB41 (MTCC#2)

<400> 22
Met Asp Phe Gly Leu Leu Pro Pro Glu Val Asn Ser Ser Arg Met Tyr
1 5 10 15
Ser Gly Pro Gly Pro Glu Ser Met Leu Ala Ala Ala Ala Ala Trp Asp
20 25 30

Gly	Val	Ala	Ala	Glu	Leu	Thr	Ser	Ala	Ala	Val	Ser	Tyr	Gly	Ser	Val
	35						40					45			
Val	Ser	Thr	Leu	Ile	Val	Glu	Pro	Trp	Met	Gly	Pro	Ala	Ala	Ala	Ala
	50					55					60				
Met	Ala	Ala	Ala	Ala	Thr	Pro	Tyr	Val	Gly	Trp	Leu	Ala	Ala	Thr	Ala
	65				70					75					80
Ala	Leu	Ala	Lys	Glu	Thr	Ala	Thr	Gln	Ala	Arg	Ala	Ala	Ala	Glu	Ala
			85					90						95	
Phe	Gly	Thr	Ala	Phe	Ala	Met	Thr	Val	Pro	Pro	Ser	Leu	Val	Ala	Ala
		100						105					110		
Asn	Arg	Ser	Arg	Leu	Met	Ser	Leu	Val	Ala	Ala	Asn	Ile	Leu	Gly	Gln
	115						120					125			
Asn	Ser	Ala	Ala	Ile	Ala	Ala	Thr	Gln	Ala	Glu	Tyr	Ala	Glu	Met	Trp
	130				135						140				
Ala	Gln	Asp	Ala	Ala	Val	Met	Tyr	Ser	Tyr	Glu	Gly	Ala	Ser	Ala	Ala
	145				150					155					160
Ala	Ser	Ala	Leu	Pro	Pro	Phe	Thr	Pro	Pro	Val	Gln	Gly	Thr	Gly	Pro
			165					170						175	
Ala	Gly	Pro	Ala	Ala	Ala	Ala	Ala	Thr	Gln	Ala	Ala	Gly	Ala	Gly	
		180					185						190		
Ala	Val	Ala	Asp	Ala	Gln	Ala	Thr	Leu	Ala	Gln	Leu	Pro	Pro	Gly	Ile
	195						200					205			
Leu	Ser	Asp	Ile	Leu	Ser	Ala	Leu	Ala	Ala	Asn	Ala	Asp	Pro	Leu	Thr
	210					215					220				
Ser	Gly	Leu	Leu	Gly	Ile	Ala	Ser	Thr	Leu	Asn	Pro	Gln	Val	Gly	Ser
	225				230					235					240
Ala	Gln	Pro	Ile	Val	Ile	Pro	Thr	Pro	Ile	Gly	Glu	Leu	Asp	Val	Ile
			245					250						255	
Ala	Leu	Tyr	Ile	Ala	Ser	Ile	Ala	Thr	Gly	Ser	Ile	Ala	Leu	Ala	Ile
		260						265					270		
Thr	Asn	Thr	Ala	Arg	Pro	Trp	His	Ile	Gly	Leu	Tyr	Gly	Asn	Ala	Gly
	275						280					285			
Gly	Leu	Gly	Pro	Thr	Gln	Gly	His	Pro	Leu	Ser	Ser	Ala	Thr	Asp	Glu
	290				295						300				
Pro	Glu	Pro	His	Trp	Gly	Pro	Phe	Gly	Gly	Ala	Ala	Pro	Val	Ser	Ala
	305				310					315					320
Gly	Val	Gly	His	Ala	Ala	Leu	Val	Gly	Ala	Leu	Ser	Val	Pro	His	Ser
			325						330					335	
Trp	Thr	Thr	Ala	Ala	Pro	Glu	Ile	Gln	Leu	Ala	Val	Gln	Ala	Thr	Pro
			340					345					350		
Thr	Phe	Ser	Ser	Ser	Ala	Gly	Ala	Asp	Pro	Thr	Ala	Leu	Asn	Gly	Met
		355					360					365			
Pro	Ala	Gly	Leu	Leu	Ser	Gly	Met	Ala	Leu	Ala	Ser	Leu	Ala	Ala	Arg
	370					375					380				
Gly	Thr	Thr	Gly	Gly	Gly	Gly	Thr	Arg	Ser	Gly	Thr	Ser	Thr	Asp	Gly
	385				390					395				400	
Gln	Glu	Asp	Gly	Arg	Lys	Pro	Pro	Val	Val	Val	Ile	Arg	Glu	Gln	Pro
			405					410						415	
Pro	Pro	Gly	Asn	Pro	Pro	Arg									
			420												

<210> 23
 <211> 154
 <212> DNA
 <213> Mycobacterium tuberculosis

<220>
 <223> ESAT-6

<400> 23
atgacagagc agcagtggaa tttcgcgggt atcgaggccg cggcaagcgc aatccaggga 60
aatgtcacgt ccattcattc cctccttgac gaggggaagc agtccctgac caagctcgca 120
gcggcctggg gcggtagcgg ttcggaagcg tacc 154

<210> 24
<211> 51
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> ESAT-6

<400> 24
Met Thr Glu Gln Gln Trp Asn Phe Ala Gly Ile Glu Ala Ala Ala Ser
1 5 10 15
Ala Ile Gln Gly Asn Val Thr Ser Ile His Ser Leu Leu Asp Glu Gly
20 25 30
Lys Gln Ser Leu Thr Lys Leu Ala Ala Trp Gly Gly Ser Gly Ser
35 40 45
Glu Ala Tyr
50

<210> 25
<211> 851
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> MTB39 (TbH9) cDNA

<400> 25
ctgcagggtg gcgtggatga gcgtcaccgc ggggcaggcc gagctgaccg ccgcccaggt 60
ccgggttgct gcggcggcct acgagacggc gtatgggctg acggtgcccc cgccgggtgat 120
cgccgagaac cgtgctgaac tgatgattct gatagcgacc aacctcttg ggcaaaacac 180
cccggcgatc gcgggtcaacg aggccgaata cggcgagatg tgggccaag acgccgccgc 240
gatgtttggc tacgccgcgg cgacggcgac ggcgacggcg acgttgctgc cgttcgagga 300
ggcgccggag atgaccagcg cgggtgggct cctcgagcag gccgccgcgg tcgaggaggc 360
ctccgacacc gccgcggcga accagttgat gaacaatgtg ccccaggcgc tgaaacagtt 420
ggcccagccc acgcagggca ccacgccttc ttccaagctg ggtggcctgt ggaagacggt 480
ctcgccgcac cggtcgccga tcagcaacat ggtgtcgatg gccaacaacc acatgtcgat 540
gaccaactcg ggtgtgtcga tgaccaacac cttgagctcg atgttgaagg gctttgctcc 600
ggcgccggcc gccaggccg tgcaaaccgc ggcgcaaaac ggggtccggg cgatgagctc 660
gctgggcagc tcgctgggtt cttcgggtct gggcggtggg gtggccgcca acttgggtcg 720
ggcggcctcg gtacggtatg gtcaccggga tggcggaata tatgcanagt ctggtcggcg 780
gaacggtggt ccggcgtaag gtttaccgcc gttttctgga tgcggtgaac ttcgtcaacg 840
gaaacagtta c 851

<210> 26
<211> 263
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> MTB39 (TbH9)

<400> 26
Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu Thr Ala Ala
1 5 10 15
Gln Val Arg Val Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu Thr
20 25 30
Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile Leu
35 40 45
Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val Asn
50 55 60
Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Ala Met Phe
65 70 75 80
Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Leu Leu Pro Phe
85 90 95
Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln Ala
100 105 110
Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn Gln Leu Met
115 120 125
Asn Asn Val Pro Gln Ala Leu Lys Gln Leu Ala Gln Pro Thr Gln Gly
130 135 140
Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser Pro
145 150 155 160
His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His Met
165 170 175
Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser Met
180 185 190
Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala Gln Ala Val Gln Thr Ala
195 200 205
Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu Gly
210 215 220
Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu Gly Arg Ala Ala
225 230 235 240
Ser Val Arg Tyr Gly His Arg Asp Gly Gly Lys Tyr Ala Xaa Ser Gly
245 250 255
Arg Arg Asn Gly Gly Pro Ala
260

<210> 27
<211> 474
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<221> CDS
<222> (16)..(450)
<223> alpha-crystalline antigen

<400> 27
attaggaggc atcaa atg gcc acc acc ctt ccc gtt cag cgc cac ccg cgg 51
Met Ala Thr Thr Leu Pro Val Gln Arg His Pro Arg
1 5 10
tcc ctc ttc ccc gag ttt tct gag ctg ttc gcg gcc ttc ccg tca ttc 99
Ser Leu Phe Pro Glu Phe Ser Glu Leu Phe Ala Ala Phe Pro Ser Phe
15 20 25
gcc gga ctc cgg ccc acc ttc gac acc cgg ttg atg cgg ctg gaa gac 147
Ala Gly Leu Arg Pro Thr Phe Asp Thr Arg Leu Met Arg Leu Glu Asp
30 35 40

gag atg aaa gag ggg cgc tac gag gta cgc gcg gag ctt ccc ggg gtc 195
 Glu Met Lys Glu Gly Arg Tyr Glu Val Arg Ala Glu Leu Pro Gly Val
 45 50 55 60

 gac ccc gac aag gac gtc gac att atg gtc cgc gat ggt cag ctg acc 243
 Asp Pro Asp Lys Asp Val Asp Ile Met Val Arg Asp Gly Gln Leu Thr
 65 70 75

 atc aag gcc gag cgc acc gag cag aag gac ttc gac ggt cgc tcg gaa 291
 Ile Lys Ala Glu Arg Thr Glu Gln Lys Asp Phe Asp Gly Arg Ser Glu
 80 85 90

 ttc gcg tac ggt tcc ttc gtt cgc acg gtg tcg ctg ccg gta ggt gct 339
 Phe Ala Tyr Gly Ser Phe Val Arg Thr Val Ser Leu Pro Val Gly Ala
 95 100 105

 gac gag gac gac att aag gcc acc tac gac aag ggc att ctt act gtg 387
 Asp Glu Asp Asp Ile Lys Ala Thr Tyr Asp Lys Gly Ile Leu Thr Val
 110 115 120

 tcg gtg gcg gtt tcg gaa ggg aag cca acc gaa aag cac att cag atc 435
 Ser Val Ala Val Ser Glu Gly Lys Pro Thr Glu Lys His Ile Gln Ile
 125 130 135 140

 cgg tcc acc aac tga ccactggggtc cgtgctgatg accg 474
 Arg Ser Thr Asn
 145

<210> 28
 <211> 144
 <212> PRT
 <213> Mycobacterium tuberculosis

<220>
 <223> alpha-crystalline antigen

<400> 28
 Met Ala Thr Thr Leu Pro Val Gln Arg His Pro Arg Ser Leu Phe Pro
 1 5 10 15
 Glu Phe Ser Glu Leu Phe Ala Ala Phe Pro Ser Phe Ala Gly Leu Arg
 20 25 30
 Pro Thr Phe Asp Thr Arg Leu Met Arg Leu Glu Asp Glu Met Lys Glu
 35 40 45
 Gly Arg Tyr Glu Val Arg Ala Glu Leu Pro Gly Val Asp Pro Asp Lys
 50 55 60
 Asp Val Asp Ile Met Val Arg Asp Gly Gln Leu Thr Ile Lys Ala Glu
 65 70 75 80
 Arg Thr Glu Gln Lys Asp Phe Asp Gly Arg Ser Glu Phe Ala Tyr Gly
 85 90 95
 Ser Phe Val Arg Thr Val Ser Leu Pro Val Gly Ala Asp Glu Asp Asp
 100 105 110
 Ile Lys Ala Thr Tyr Asp Lys Gly Ile Leu Thr Val Ser Val Ala Val
 115 120 125
 Ser Glu Gly Lys Pro Thr Glu Lys His Ile Gln Ile Arg Ser Thr Asn
 130 135 140

<400> 29																	
aggtgtccgg		gccgacgctg		aatcgtttagc		caaccgcgat		ctcgcgctgc		ggccacgaca		60					
ttcgaactga		gcgtcctcgg		tgtgtttcac		tcgcccagaa		cagattcgcac		cgcgctcgtgc		120					
gcagatgaga		gttgggattg		gtagtagct		atg		acg	ttc	ttc	gaa	cag	gtg	cga	173		
						Met		Thr	Phe	Phe	Glu	Gln	Val	Arg			
						1				5							
agg		ttg	cgg	agc	gca	gcg	aca	acc	ctg	ccg	cgc	cgc	gtg	gct	atc	gcg	221
Arg		Leu	Arg	Ser	Ala	Ala	Thr	Thr	Leu	Pro	Arg	Arg	Val	Ala	Ile	Ala	
10						15				20							
gct		atg	ggg	gct	gtc	ctg	gtt	tac	ggc	ctg	gtc	ggc	acc	ttc	ggc	ggg	269
Ala		Met	Gly	Ala	Val	Leu	Val	Tyr	Gly	Leu	Val	Gly	Thr	Phe	Gly	Gly	
25						30				35		40					
ccg		gcc	acc	gcg	ggc	gca	ttc	tct	agg	ccc	ggc	ctt	cca	gtg	gaa	tat	317
Pro		Ala	Thr	Ala	Gly	Ala	Phe	Ser	Arg	Pro	Gly	Leu	Pro	Val	Glu	Tyr	
				45				50				55					
ctg		cag	gtg	cca	tcc	gcg	tcg	atg	ggc	cgc	gac	atc	aag	gtc	cag	ttc	365
Leu		Gln	Val	Pro	Ser	Ala	Ser	Met	Gly	Arg	Asp	Ile	Lys	Val	Gln	Phe	
				60				65				70					
cag		ggc	ggc	gga	ccg	cac	gcg	gtc	tac	ctg	ctc	gac	ggc	ctg	cgg	gcc	413
Gln		Gly	Gly	Gly	Pro	His	Ala	Val	Tyr	Leu	Leu	Asp	Gly	Leu	Arg	Ala	
		75						80				85					
cag		gat	gac	tac	aac	ggc	tgg	gac	atc	aac	acc	ccg	gcc	ttc	gag	gag	461
Gln		Asp	Asp	Tyr	Asn	Gly	Trp	Asp	Ile	Asn	Thr	Pro	Ala	Phe	Glu	Glu	
		90				95						100					
tac		tac	cag	tca	ggg	ttg	tcg	gtg	atc	atg	ccc	gtg	ggc	ggc	caa	tcc	509
Tyr		Tyr	Gln	Ser	Gly	Leu	Ser	Val	Ile	Met	Pro	Val	Gly	Gly	Gln	Ser	
105						110				115		120					
agt		ttc	tac	acc	gac	tgg	tat	cag	ccc	tcg	cag	agc	aac	ggc	cag	aac	557
Ser		Phe	Tyr	Thr	Asp	Trp	Tyr	Gln	Pro	Ser	Gln	Ser	Asn	Gly	Gln	Asn	
				125				130						135			
tac		acc	tac	aag	tgg	gag	acc	ttc	ctt	acc	aga	gag	atg	ccc	gcc	tgg	605
Tyr		Thr	Tyr	Lys	Trp	Glu	Thr	Phe	Leu	Thr	Arg	Glu	Met	Pro	Ala	Trp	
				140				145				150					
cta		cag	gcc	aac	aag	ggc	gtg	tcc	ccg	aca	ggc	aac	gcg	gcg	gtg	ggc	653
Leu		Gln	Ala	Asn	Lys	Gly	Val	Ser	Pro	Thr	Gly	Asn	Ala	Ala	Val	Gly	
		155				160						165					

ctt tgc atg tgc ggc ggt tcc gcg ctg atc ctg gcc gcg tac tac ccg	701
Leu Ser Met Ser Gly Gly Ser Ala Leu Ile Leu Ala Ala Tyr Tyr Pro	
170 175 180	
cag cag ttc ccg tac gcc gcg tgc ttg tgc ggc ttc ctc aac ccg tcc	749
Gln Gln Phe Pro Tyr Ala Ala Ser Leu Ser Gly Phe Leu Asn Pro Ser	
185 190 195 200	
gag ggc tgg tgg ccg acg ctg atc ggc ctg gcg atg aac gac tgc ggc	797
Glu Gly Trp Trp Pro Thr Leu Ile Gly Leu Ala Met Asn Asp Ser Gly	
205 210 215	
ggt tac aac gcc aac agc atg tgg ggt ccg tcc agc gac ccg gcc tgg	845
Gly Tyr Asn Ala Asn Ser Met Trp Gly Pro Ser Ser Asp Pro Ala Trp	
220 225 230	
aag cgc aac gac cca atg gtt cag att ccc cgc ctg gtc gcc aac aac	893
Lys Arg Asn Asp Pro Met Val Gln Ile Pro Arg Leu Val Ala Asn Asn	
235 240 245	
acc cgg atc tgg gtg tac tgc ggt aac ggc aca ccc agc gac ctc ggc	941
Thr Arg Ile Trp Val Tyr Cys Gly Asn Gly Thr Pro Ser Asp Leu Gly	
250 255 260	
ggc gac aac ata ccg gcg aag ttc ctg gaa ggc ctc acc ctg cgc acc	989
Gly Asp Asn Ile Pro Ala Lys Phe Leu Glu Gly Leu Thr Leu Arg Thr	
265 270 275 280	
aac cag acc ttc ccg gac acc tac gcg gcc gac ggt gga cgc aac ggg	1037
Asn Gln Thr Phe Arg Asp Thr Tyr Ala Ala Asp Gly Gly Arg Asn Gly	
285 290 295	
gtg ttt aac ttc ccg ccc aac gga aca cac tgc tgg ccc tac tgg aac	1085
Val Phe Asn Phe Pro Pro Asn Gly Thr His Ser Trp Pro Tyr Trp Asn	
300 305 310	
gag cag ctg gtc gcc atg aag gcc gat atc cag cat gtg ctc aac ggc	1133
Glu Gln Leu Val Ala Met Lys Ala Asp Ile Gln His Val Leu Asn Gly	
315 320 325	
gcg aca ccc ccg gcc gcc cct gct gcg ccg gcc gcc tga gccagcaagc	1182
Ala Thr Pro Pro Ala Ala Pro Ala Ala Pro Ala Ala	
330 335 340	
cagcatcggc agcagcgcaa cggccagcg	1211

<210> 30

<211> 340

<212> PRT

<213> Mycobacterium tuberculosis

<220>

<223> 85 complex antigen (MTB85 complex antigen)

<400> 30

Met Thr Phe Phe Glu Gln Val Arg Arg Leu Arg Ser Ala Ala Thr Thr	
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Leu Pro Arg Arg Val Ala Ile Ala Ala Met Gly Ala Val Leu Val Tyr	
20 25 30	

Gly	Leu	Val	Gly	Thr	Phe	Gly	Gly	Pro	Ala	Thr	Ala	Gly	Ala	Phe	Ser
	35						40					45			
Arg	Pro	Gly	Leu	Pro	Val	Glu	Tyr	Leu	Gln	Val	Pro	Ser	Ala	Ser	Met
	50					55					60				
Gly	Arg	Asp	Ile	Lys	Val	Gln	Phe	Gln	Gly	Gly	Gly	Pro	His	Ala	Val
	65				70					75					80
Tyr	Leu	Leu	Asp	Gly	Leu	Arg	Ala	Gln	Asp	Asp	Tyr	Asn	Gly	Trp	Asp
			85						90					95	
Ile	Asn	Thr	Pro	Ala	Phe	Glu	Glu	Tyr	Tyr	Gln	Ser	Gly	Leu	Ser	Val
			100					105					110		
Ile	Met	Pro	Val	Gly	Gly	Gln	Ser	Ser	Phe	Tyr	Thr	Asp	Trp	Tyr	Gln
			115					120				125			
Pro	Ser	Gln	Ser	Asn	Gly	Gln	Asn	Tyr	Thr	Tyr	Lys	Trp	Glu	Thr	Phe
	130					135					140				
Leu	Thr	Arg	Glu	Met	Pro	Ala	Trp	Leu	Gln	Ala	Asn	Lys	Gly	Val	Ser
	145				150					155					160
Pro	Thr	Gly	Asn	Ala	Ala	Val	Gly	Leu	Ser	Met	Ser	Gly	Gly	Ser	Ala
			165					170						175	
Leu	Ile	Leu	Ala	Ala	Tyr	Tyr	Pro	Gln	Phe	Pro	Tyr	Ala	Ala	Ser	
			180					185				190			
Leu	Ser	Gly	Phe	Leu	Asn	Pro	Ser	Glu	Gly	Trp	Trp	Pro	Thr	Leu	Ile
		195				200						205			
Gly	Leu	Ala	Met	Asn	Asp	Ser	Gly	Gly	Tyr	Asn	Ala	Asn	Ser	Met	Trp
	210				215					220					
Gly	Pro	Ser	Ser	Asp	Pro	Ala	Trp	Lys	Arg	Asn	Asp	Pro	Met	Val	Gln
	225				230					235					240
Ile	Pro	Arg	Leu	Val	Ala	Asn	Asn	Thr	Arg	Ile	Trp	Val	Tyr	Cys	Gly
			245					250						255	
Asn	Gly	Thr	Pro	Ser	Asp	Leu	Gly	Gly	Asp	Asn	Ile	Pro	Ala	Lys	Phe
			260					265					270		
Leu	Glu	Gly	Leu	Thr	Leu	Arg	Thr	Asn	Gln	Thr	Phe	Arg	Asp	Thr	Tyr
		275					280					285			
Ala	Ala	Asp	Gly	Gly	Arg	Asn	Gly	Val	Phe	Asn	Phe	Pro	Pro	Asn	Gly
	290					295					300				
Thr	His	Ser	Trp	Pro	Tyr	Trp	Asn	Glu	Gln	Leu	Val	Ala	Met	Lys	Ala
	305				310					315					320
Asp	Ile	Gln	His	Val	Leu	Asn	Gly	Ala	Thr	Pro	Pro	Ala	Ala	Pro	Ala
				325				330						335	
Ala	Pro	Ala	Ala												
			340												